

STIC-Biotech/ChemLib

165712

From: Bowman, Amy
Sent: Wednesday, September 14, 2005 2:24 PM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/738,413

Hello,
I need SEQ ID NO: 1 in application 10/738,413 searched, length limited to 21 nucleotides.
Thank you,
Amy Bowman
AU 1635
mail REM 2C18
REM 2C31
571-272-0755

CRPG

EDWARD HART

9/19/05

9/15/05

1-NA
01

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art found, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not** found:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop-off or send completed forms to STIC Biotech-Chem Library, Remsen Bldg.



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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 09:08:30 ; Search time 1540 Seconds

(without alignments)
660.753 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 usagaccgcagcagucucut 21

Scoring table: IDENTITY_NUC

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 892778

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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11: gb_sbs:*
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13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.2	62.9	19	4	DOG2P2402
2	12.8	61.0	20	6	AR125581
3	12.8	61.0	21	6	BD171375
4	12.8	61.0	21	6	BD173609
5	12.4	59.0	19	12	AB069169
6	12.4	59.0	20	6	AR315617
7	12.4	59.0	20	6	AX462804
8	12.2	58.1	20	6	AR257223
9	12.2	58.1	20	6	AR257223
10	12.2	57.1	17	6	AX294943
11	12.2	57.1	17	6	AX264519
12	12.2	57.1	17	6	AX264520
13	12.2	57.1	17	6	AX264523
14	12.2	57.1	17	6	AX264524
15	12.2	57.1	17	6	AX687762
16	12.2	57.1	17	6	AX687763
17	12.2	57.1	17	6	AX687764
18	12.2	57.1	17	6	AX687765
19	12.2	57.1	17	6	AX687766

20	12	57.1	20	6	AX62811
21	12	57.1	21	6	AR123316
22	12	57.1	21	6	AR487412
23	12	57.1	21	6	AR529674
24	12	57.1	21	6	AX095699
25	11.8	56.2	17	6	AX726633
26	11.8	56.2	17	6	AX757199
27	11.8	56.2	20	6	CQ873538
28	11.8	56.2	20	6	AR221414
29	11.8	56.2	20	6	AR230996
30	11.8	56.2	20	6	AR271825
31	11.8	56.2	20	6	AR477925
32	11.8	56.2	21	6	AR530156
33	11.8	56.2	21	6	AX096181
34	11.6	55.2	20	6	AR067013
35	11.6	55.2	20	6	AR150409
36	11.6	55.2	20	6	BD228282
37	11.6	55.2	20	6	AR231077
38	11.6	55.2	20	6	AR312358
39	11.6	55.2	20	6	AX378632
40	11.4	54.3	13	6	E14819
41	11.4	54.3	16	6	AX255813
42	11.4	54.3	17	6	I26890
43	11.4	54.3	17	6	I91631
44	11.4	54.3	17	6	AR286107
45	11.4	54.3	17	6	AR286487

ALIGNMENTS

RESULT 1
DOG2P2402/c 19 bp DNA linear MAM 11-JUN-1993
LOCUS Dog (Clone: CXK.204) primer for STS 204, 3' end.
DEFINITION L15665
ACCESSION L15665
VERSION L15665.1 GI:290145
KEYWORDS PCR identification; PCR primer; STS.
SEGMENT 2 of 2
SOURCE
ORGANISM Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE
AUTHORS Ostrander, E.A., Sprague, G.F., Jr. and Rine, J.D.
TITLE Identification and characterization of dinucleotide repeat (CA)n markers for genetic mapping in dog
JOURNAL Genomics (1993) In press
COMMENT Original source text: Canis familiaris (library: E. Ostrander, in pBluescript+) adult spleen DNA.
Submitted by: Human Genome Center,
Lawrence Berkeley Laboratory,
1 Cyclotron Road, Berkeley, CA 94720, USA
e-mail: EOstrander@lbl.gov

PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
Annealing: 55 or 59 degrees C for 0.45 minutes
Polymerization: 74 degrees C for 1.00 minutes
PCR Cycles: 33
Final Extension: 74 degrees C for 5.00 minutes.

FEATURES
Location/Qualifiers

1..19
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
/feature_type="spleen"
/dev_stage="adult"
/cbase_lib="E. Ostrander, in pBluescript+"
complement(1..19)
/evidence=experimental

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Best Local Similarity 72.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 4 GACCGCCAGGCGUCU 21
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Db 19 GACCTGCCAGCAGCTTT 2

RESULT 2
AR125581 20 bp DNA linear PAT 16-MAY-2001
LOCUS AR125581
DEFINITION Sequence 82 from patent US 6177273.
ACCESSION AR125581
VERSION AR125581.1 GI:14111643
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 20)
TITLE Bennett,C.Frank. and Cowser,L.M.
JOURNAL Antisense modulation of integrin-linked kinase expression
PATENT: US 6177273-A 82 23-JAN-2001;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

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Best Local Similarity 68.8%; Pred. No. 4.2e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 AGGACCGCCAGGCGU 17
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Db 3 AGGACCTTCCAGTCTT 18

RESULT 3
BD171375 21 bp DNA linear PAT 18-FEB-2003
LOCUS BD171375
DEFINITION Method for detecting bronchial asthma risk factor.
ACCESSION BD171375
VERSION BD171375.1 GI:28412665
KEYWORDS JP 2002218997-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1 (bases 1 to 21)
AUTHORS Nakamura,Y. and Tamari,M.
TITLE Method for detecting bronchial asthma risk factor
JOURNAL Patent: JP 2002218997-A 10 06-AUG-2002;
OTSUKA PHARMACEUTICAL CO LTD
COMMENT OS Artificial Sequence
PN JP 2002218997-A/10
PD 06-AUG-2002
PF 25-JAN-2001 JP 2001017076
PI YUSUKE NAKAMURA,MAYUMI TAMARI
PC C12Q1/68,C12N15/09,C12N15/00
CC Primer sequence (FS) for PCR
FH Key Location/Qualifiers
FT source 1..21
Location/Qualifiers
1..21
/organism='Artificial Sequence'.
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source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 61.0%; Score 12.8; DB 6; Length 21;
Best Local Similarity 62.5%; Pred. No. 4.2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACCGCGCAGGCGUCU 20
||||:||||:|:|
Db 5 ACCGCGCAGGTCTTTT 20

RESULT 4
BD173609 21 bp DNA linear PAT 18-FEB-2003
LOCUS BD173609
DEFINITION Method of detecting bronchial asthma onset risk factor.
ACCESSION BD173609
VERSION BD173609.1 GI:28414940
KEYWORDS WO 02059305-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1 (bases 1 to 21)
AUTHORS Nakamura,Y. and Tamari,M.
TITLE Method of detecting bronchial asthma onset risk factor
JOURNAL Patent: WO 02059305-A 10 01-AUG-2002;
OTSUKA PHARMACEUTICAL CO LTD,YUSUKE NAKAMURA,MAYUMI TAMARI
COMMENT OS Artificial Sequence
PN WO 02059305-A/10
PD 01-AUG-2002
PF 25-JAN-2002 WO 2002JP000540
PR 25-JAN-2001 JP 01P 017076
PI YUSUKE NAKAMURA,MAYUMI TAMARI
PC C12N15/12,C12Q1/68,G01N33/53
CC Primer sequence (FS) for PCR
FH Key Location/Qualifiers
FT source 1..21
Location/Qualifiers
1..21
/organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 61.0%; Score 12.8; DB 6; Length 21;
Best Local Similarity 62.5%; Pred. No. 4.2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 5 ACCGCGCAGGCGUCU 20
||||:||||:|:|
Db 5 ACCGCGCAGGTCTTTT 20

RESULT 5
AB069169 19 bp DNA linear SYN 21-MAY-2003
LOCUS AB069169
DEFINITION Synthetic construct DNA, reverse primer for human SRS ets-R-100A7R
at 1p36.
ACCESSION AB069169
VERSION AB069169.1 GI:15129973
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1 (bases 1 to 19)
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
Watanabe,N., Inazawa,T., Hosoda,F., Arai,Y., Mizushima,H.,
Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
TITLE A BAC-based SRS-content map spanning a 35-Mb region of human
chromosome 1p35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE
2 (bases 1 to 19)
AUTHORS Horii,A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology, 2-1 Seiryomachi, Aoba-ku, Sendai,

ORIGIN
Query Match 61.0%; Score 12.8; DB 6; Length 21;
Best Local Similarity 62.5%; Pred. No. 4.2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Miyagi 980-8575, Japan (E-mail:horie@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)

FEATURES
source

1. .19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
misc_feature
1. .19
/note="reverse primer for human STS sts-R-100A7R at 1p36
sts-R-100A7R obtained from clones B100A7, Human BAC
library RPCI-11"

ORIGIN

Query Match 59.0%; Score 12.4; DB 12; Length 19;
Best Local Similarity 85.7%; Pred. No. 7.1e+04;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 AGACCGCCGAG 15
DB 3 AGACCTGCCAG 16

RESULT 6
LOCUS AR315617 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6154 from patent US 6559294.
ACCESSION AR315617
VERSION AR315617.1 GI:31709043
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
Griffiths, R., Holseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
Sankaran, B., and Fletcher, L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 6154 06-MAY-2003;
LOCATION/Qualifiers
1. .20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 59.0%; Score 12.4; DB 6; Length 20;
Best Local Similarity 64.3%; Pred. No. 7.1e+04;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 8 UGCCAGUCGUCU 21
DB 15 TGCTGTGCTCTT 2

RESULT 7
LOCUS AX462804/c 20 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 548 from Patent EP1217079.
ACCESSION AX462804
VERSION AX462804.1 GI:21866030
KEYWORDS
SOURCE Aegilops tauschii
ORGANISM Aegilops tauschii
REFERENCE
1
Bernard, M., Sourdil, P., and Guyomarch, H.
Microsatellite markers from Triticum tauschii
Patent: EP 1217079-A 548 26-JUN-2002;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
LOCATION/Qualifiers
1. .20
/organism="Aegilops tauschii"
/mol_type="unassigned DNA"

FEATURES
source

/db_xref="taxon:37682"

ORIGIN

Query Match 59.0%; Score 12.4; DB 6; Length 20;
Best Local Similarity 78.6%; Pred. No. 7.1e+04;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 AGACCGCCGAG 15
DB 18 AGACCTGCCATTG 5

RESULT 8
LOCUS AR257223/c 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 78 from patent US 6485974.
ACCESSION AR257223
VERSION AR257223.1 GI:27307007
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
Popoff, I.
Antisense modulation of PTPN2 expression
Patent: US 6485974-A 78 26-NOV-2002;
LOCATION/Qualifiers
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/organism="unknown"
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Best Local Similarity 58.8%; Pred. No. 9.3e+04;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 UAGACCGCCGAGCU 17
DB 20 TAGTACTGACAGTCT 4

RESULT 9
LOCUS AX294943 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 6705 from Patent WO0179548.
ACCESSION AX294943
VERSION AX294943.1 GI:17056626
KEYWORDS
SOURCE Synthetic construct
ORGANISM Synthetic construct
REFERENCE
1
Barany, F., Ziv, M., Gerry, N.P., Favis, R., and Kliman, R.
Method of designing addressable array for detection of nucleic acid
Sequence differences using ligase detection reaction
Patent: WO 0179548-A 6705 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
LOCATION/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

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Best Local Similarity 64.7%; Pred. No. 9.3e+04;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 4 GACCTCCGCGCCTT 20
DB 4 GACCTCCGCGCCTT 20

FEATURES
source

RESULT 10
AX264519/c
LOCUS AX264519 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 1910 from Patent WO0173002.
ACCESSION AX264519
VERSION AX264519.1 GI:16513318
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 1910 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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source Location/Qualifiers
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/db_xref="taxon:9606"
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Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 AGGACCTGCCAG 13
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Db 16 AGGACCTGCCAG 5
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RESULT 11
AX264520 17 bp DNA linear PAT 26-OCT-2001
LOCUS AX264520
DEFINITION Sequence 1911 from Patent WO0173002.
ACCESSION AX264520
VERSION AX264520.1 GI:16513319
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 1911 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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Db 2 AGGACCTGCCAG 13
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RESULT 12
AX264523/c 17 bp DNA linear PAT 26-OCT-2001
LOCUS AX264523
DEFINITION Sequence 1914 from Patent WO0173002.
ACCESSION AX264523
VERSION AX264523.1 GI:16513322

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 1914 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
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Best Local Similarity 91.7%; Pred. No. 1.2e+05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 AGGACCTGCCAG 13
|||||:|||||
Db 12 AGGACCTGCCAG 1
|||||:|||||
RESULT 13
AX264524 17 bp DNA linear PAT 26-OCT-2001
LOCUS AX264524
DEFINITION Sequence 1915 from Patent WO0173002.
ACCESSION AX264524
VERSION AX264524.1 GI:16513323
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 1915 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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Best Local Similarity 91.7%; Pred. No. 1.2e+05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 AGGACCTGCCAG 13
|||||:|||||
Db 6 AGGACCTGCCAG 17
|||||:|||||
RESULT 14
AX687762/c 17 bp DNA linear PAT 31-MAR-2003
LOCUS AX687762
DEFINITION Sequence 494 from Patent EP1281758.
ACCESSION AX687762
VERSION AX687762.1 GI:29410458
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.

TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and

JOURNAL mdz12 Patent: EP 1281758-A 494 05-FEB-2003;

FEATURES Aeomica, Inc. (US)

source Location/Qualifiers

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

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Best Local Similarity 75.0%; Pred. No. 1.2e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCAGUGCUCCTT 21
|||:|:|:|
Db 17 CCAGTGTCTTT 6

RESULT 15

AX687763/c 17 bp DNA linear PAT 31-MAR-2003

LOCUS Sequence 495 from Patent EP1281758.

DEFINITION AX687763

ACCESSION AX687763.1 GI:29410459

VERSION

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.

TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and

JOURNAL mdz12 Patent: EP 1281758-A 495 05-FEB-2003;

FEATURES Aeomica, Inc. (US)

source Location/Qualifiers

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Db 16 CCAGTGTCTTT 5

Search completed: September 17, 2005, 10:47:56
Job time : 1546 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 09:06:56; Search time 256 Seconds
(without alignments)
485,604 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21
Sequence: 1 uagaccugccagugcucut 21

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 2380332

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
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2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	15	71.4	20 4	AA16582
C 2	13.6	64.8	20 12	ADP68070
C 3	13.6	64.8	20 12	ADP68033
C 4	13.2	62.9	20 12	ADH64423
C 5	13.2	62.9	20 12	ADH64554
C 6	13.2	62.9	20 12	ADH63908
C 7	12.8	61.0	17 11	ADL48810
C 8	12.8	61.0	17 11	ADL48391
C 9	12.8	61.0	19 12	ADL14399
C 10	12.8	61.0	20 4	AA16582
C 11	12.8	61.0	20 10	ADP69553
C 12	12.8	61.0	20 10	ADP69553
C 13	12.8	61.0	20 12	ADH54183
C 14	12.8	61.0	20 12	ADH54183
C 15	12.8	61.0	20 12	ADH63823
C 16	12.8	61.0	20 12	ADH63823
C 17	12.8	61.0	20 12	ADH63823
C 18	12.8	61.0	20 12	ADH63823
C 19	12.8	61.0	20 12	ADH63823
C 20	12.8	61.0	20 12	ADH63823

C 21	12.8	61.0	20 12	ADM15205	ADM15205 Human mpg
C 22	12.8	61.0	20 12	ADM14808	ADM14808 Human mpg
C 23	12.8	61.0	21 6	AA144199	AA144199 Human t-k
C 24	12.6	60.0	19 4	AA695089	AA695089 Human t-k
C 25	12.6	60.0	20 2	AA695046	AA695046 M. pneumo
C 26	12.6	60.0	20 3	AA614197	AA614197 M. pneumo
C 27	12.6	60.0	20 10	AB285113	AB285113 Human oli
C 28	12.6	60.0	20 11	ABD21343	ABD21343 Human tra
C 29	12.6	60.0	21 9	ABD58127	ABD58127 GAPDH bpe
C 30	12.6	60.0	21 10	ADDA4397	ADDA4397 Rat GAPDH
C 31	12.4	59.0	17 2	AAV95322	AAV95322 Human c-f
C 32	12.4	59.0	18 12	ADK15803	ADK15803 Human ABC
C 33	12.4	59.0	20 2	AA205318	AA205318 PCR prime
C 34	12.4	59.0	20 2	AA296828	AA296828 PCR prime
C 35	12.4	59.0	20 6	ABQ93280	ABQ93280 T. cauch
C 36	12.4	59.0	20 6	AB660954	AB660954 Human gen
C 37	12.4	59.0	20 12	ADM14770	ADM14770 Human mpg
C 38	12.4	59.0	20 12	ADM15365	ADM15365 Human mpg
C 39	12.4	59.0	20 12	ADM94834	ADM94834 Human mid
C 40	12.2	58.1	19 10	ADF37557	ADF37557 Human VEG
C 41	12.2	58.1	19 10	ADF37310	ADF37310 Human VEG
C 42	12.2	58.1	19 12	ADQ60823	ADQ60823 Ant1-IRS1
C 43	12.2	58.1	20 6	AB194985	AB194985 Capture o
C 44	12.2	58.1	20 8	AA536332	AA536332 Human ptp
C 45	12.2	58.1	20 10	ADF88187	ADF88187 Single nu

ALIGNMENTS

RESULT 1
ID AA16582 standard; DNA; 20 BP.
XX
AC AA16582;
DT 11-DEC-2001 (first entry)
XX
DE Oculocutaneous albinism 1B causative gene related PCR primer #2.
DE
XX Hamster; oculocutaneous albinism 1B; tyrosinase; OCA1B;
KW pigment sedimentation; ocular function; PCR primer; ss.
XX
XX Unidentified.
OS
XX JP2001112483-A.
PN 24-APR-2001.
PD 18-OCT-1999; 99JP-00295686.
PF 18-OCT-1999; 99JP-00295686.
XX
PR 18-OCT-1999; 99JP-00295686.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 2001-372654/39.
XX
XX An ocular-cutaneous albinism 1B causative gene and its application.
XX Example 5; Page 7; 17pp; Japanese.
XX
CC The present invention relates to a transgenic animal, particularly a
CC hamster, which has a mutant version of the oculocutaneous albinism 1B
CC (OCA1B) causative gene. The protein encoded by this gene is a tyrosinase,
CC which can be detected in the animal. It can also be used in the
CC prevention, diagnosis and treatment of OCA1B, and to investigate
CC mechanisms in pigment sedimentation and ocular function. The present
CC sequence is a PCR primer described in the exemplification of the
CC invention
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 71.4%; Score 15; DB 4; Length 20;

*Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GACCTGCCAGUCGUC 18
|||:|||||:
Db 20 GACCTGCCAGTCTC 6

RESULT 2

ADP68070/c
ID ADP68070 standard; DNA; 20 BP.

AC ADP68070;

DT 12-AUG-2004 (first entry)

DE Human jagged 1 target oligonucleotide #1.

XX Jagged 1; serrate gene; JAG 1; HJ1; AGS; AMD; AWS; diagnosis;
KW hyperproliferative disorder; developmental disorder; cytostatic; therapy;
KW human; ss.

XX Homo sapiens.

OS US2004102401-A1.

PN 27-MAY-2004.

PD 22-NOV-2002; 2002US-00304082.

PE 22-NOV-2002; 2002US-00304082.

PR 22-NOV-2002; 2002US-00304082.

PA (ISIS-) ISIS PHARM INC.

PI Dean NM, Bennett CF, Dobie KW;

DR WPI; 2004-399731/37.

XX New compound targeted to a nucleic acid molecule encoding jagged 1,
PT useful in diagnosing and treating hyperproliferative disorder.

XX Example 15; SEQ ID NO 48; 40pp; English.

XX The present invention is directed to antisense oligonucleotides targeted
CC to jagged 1 (also known as serrate gene, JAG1, HJ1, AGS, AMD and AWS) and
CC which modulate the expression of jagged 1. The invention is useful in
CC diagnosing and treating hyperproliferative and developmental disorders.
CC The invention acts as a cytostatic agent. The present sequence is human
CC jagged 1 target oligonucleotide. This sequence is used in the
CC exemplification of the invention.

XX Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 64.8%; Score 13.6; DB 12; Length 20;

Best Local Similarity 70.0%; Pred. No. 8.2e+03;

Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCTGCCAGUCGUCATT 21
|||:|||||:
Db 20 AGGACCTGCCAGGCTCATT 1

RESULT 3

ADP68033
ID ADP68033 standard; DNA; 20 BP.

AC ADP68033;

DT 12-AUG-2004 (first entry)

DE Human jagged 1 antisense oligonucleotide ISIS #171243.

XX Jagged 1; serrate gene; JAG 1; HJ1; AGS; AMD; AWS; diagnosis;
KW

KW hyperproliferative disorder; developmental disorder; cytostatic; therapy;
KW human; antisense; phosphorothioate backbone; ss.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

FT modified_base 1..20

FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone where all cytidines are

FT 5-methyl cytidines"

FT modified_base 1..5

FT /tag= a
FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 16..20

FT /tag= c
FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

OS US2004102401-A1.

PN 27-MAY-2004.

PD 22-NOV-2002; 2002US-00304082.

PE 22-NOV-2002; 2002US-00304082.

PR 22-NOV-2002; 2002US-00304082.

PA (ISIS-) ISIS PHARM INC.

PI Dean NM, Bennett CF, Dobie KW;

DR WPI; 2004-399731/37.

XX New compound targeted to a nucleic acid molecule encoding jagged 1,
PT useful in diagnosing and treating hyperproliferative disorder.

XX Example 15; SEQ ID NO 11; 40pp; English.

XX The present invention is directed to antisense oligonucleotides targeted
CC to jagged 1 (also known as serrate gene, JAG1, HJ1, AGS, AMD and AWS) and
CC which modulate the expression of jagged 1. The invention is useful in
CC diagnosing and treating hyperproliferative and developmental disorders.
CC The invention acts as a cytostatic agent. The present sequence is human
CC jagged 1 antisense oligonucleotide. This sequence is used in the
CC exemplification of the invention.

XX Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 64.8%; Score 13.6; DB 12; Length 20;

Best Local Similarity 70.0%; Pred. No. 8.2e+03;

Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCTGCCAGUCGUCATT 21
|||:|||||:
Db 1 AGGACCTGCCAGGCTCATT 20

RESULT 4

ADH64423
ID ADH64423 standard; DNA; 20 BP.

AC ADH64423;

DT 25-MAR-2004 (first entry)

DE Human glucocorticoid receptor-specific antisense oligonucleotide #1257.

XX antisense oligonucleotide; glucocorticoid receptor; infection;

KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.

XX OS Homo sapiens.
 XX PN WO2003099215-A2.
 XX PD 04-DEC-2003.
 XX PF 20-MAY-2003; 2003WO-US016084.
 XX PR 20-MAY-2002; 2002US-0381857P.
 XX PA (PHAA) PHARMACIA CORP.
 XX PI Crosby SD, Nalseeth AE;
 XX DR WPI; 2004-035034/03.
 XX SQ New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
 CC Claim 4; SEQ ID NO 1257; 985bp; English.
 CC The invention comprises an antisense oligonucleotides that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity, The
 CC cardiovascular disorders, hyperlipidemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 XX SQ Sequence 20 BP; 1 A; 7 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 12; Length 20;
 Best Local Similarity 61.1%; Pred. No. 1.3e+04;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 GACCTGCCAGGCTCTT 21
 DB 2 GTCCTTCACGCTCTTT 19

RESULT 5

ID ADH64554 standard; DNA; 20 BP.
 XX ADH64554;

AC 25-MAR-2004 (first entry)
 DT 25-MAR-2004 (first entry)

XX Human glucocorticoid receptor-specific antisense oligonucleotide #1388.
 DE Human glucocorticoid receptor-specific antisense oligonucleotide #1388.

XX antisense oligonucleotide; glucocorticoid receptor; infection;
 KW inflammation; tumour formation; diabetes; obesity;
 KW cardiovascular disorder; hyperlipidemia; Cushing's syndrome; human; ss;
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
 XX OS Homo sapiens.
 XX PN WO2003099215-A2.
 XX PD 04-DEC-2003.
 XX PF 20-MAY-2003; 2003WO-US016084.
 XX PR 20-MAY-2002; 2002US-0381857P.
 XX PA (PHAA) PHARMACIA CORP.
 XX PI Crosby SD, Nalseeth AE;
 XX DR WPI; 2004-035034/03.
 XX SQ New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
 CC Claim 4; SEQ ID NO 1257; 985bp; English.

DR WPI; 2004-035034/03.
 XX New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
 XX Claim 4; SEQ ID NO 1388; 985bp; English.
 XX The invention comprises an antisense oligonucleotides that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity, The
 CC cardiovascular disorders, hyperlipidemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 XX SQ Sequence 20 BP; 1 A; 8 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 12; Length 20;
 Best Local Similarity 61.1%; Pred. No. 1.3e+04;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 GACCTGCCAGGCTCTT 21
 DB 3 GTCCTTCACGCTCTTT 20

RESULT 6

ID ADH63908 standard; DNA; 20 BP.
 XX ADH63908;

AC 25-MAR-2004 (first entry)
 DT 25-MAR-2004 (first entry)

XX Human glucocorticoid receptor-specific antisense oligonucleotide #742.
 DE Human glucocorticoid receptor-specific antisense oligonucleotide #742.

XX antisense oligonucleotide; glucocorticoid receptor; infection;
 KW inflammation; tumour formation; diabetes; obesity;
 KW cardiovascular disorder; hyperlipidemia; Cushing's syndrome; human; ss;
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
 XX OS Homo sapiens.
 XX PN WO2003099215-A2.
 XX PD 04-DEC-2003.
 XX PF 20-MAY-2003; 2003WO-US016084.
 XX PR 20-MAY-2002; 2002US-0381857P.
 XX PA (PHAA) PHARMACIA CORP.
 XX PI Crosby SD, Nalseeth AE;
 XX DR WPI; 2004-035034/03.
 XX SQ New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
 CC Claim 4; SEQ ID NO 742; 985bp; English.

The invention comprises an antisense oligonucleotides that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity, The
 CC cardiovascular disorders, hyperlipidemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets

CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 1 A; 7 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 12; Length 20;
Best Local Similarity 61.1%; Pred. No. 1.3e+04;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 GACCGGCGAGGCGUCUTT 21
| | | | | : | | : | | : | |
Db 1 GTCTTCACACTGCTCTTT 18

RESULT 7
ADL48810
ID ADL48810 standard; RNA, 17 BP.

AC ADL48810;

DT 20-MAY-2004 (first entry)

DE Human IKK-gamma substrate sequence #1320.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW resectosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; Human IKK-gamma;
KW substrate; ds.

XX unidentified.

XX WO200281628-A2.

PD 17-OCT-2002.

PF 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

PR 29-MAY-2001; 2001US-0294412P.

PR 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

PI Blatt L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;

DR WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PI protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 2343; 317bp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC resectosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a

CC target RNA in a cell. The present RNA sequence represents a human IKK-
CC gamma substrate sequence.

XX
SQ Sequence 17 BP; 2 A; 5 C; 8 G; 0 T; 2 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 11; Length 17;
Best Local Similarity 87.5%; Pred. No. 2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 UAGGACCGGCGGCGC 16
| | | | | | | | | | | | | |
Db 2 UAGGACCGGCGGCGC 17

RESULT 8
ADL48391
ID ADL48391 standard; RNA, 17 BP.

AC ADL48391;

DT 20-MAY-2004 (first entry)

DE Human IKK-gamma substrate sequence #901.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW resectosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; Human IKK-gamma;
KW substrate; ds.

XX unidentified.

XX WO200281628-A2.

PD 17-OCT-2002.

PF 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

PR 29-MAY-2001; 2001US-0294412P.

PR 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

PI Blatt L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;

DR WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PI protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 1924; 317bp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC resectosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a

CC target RNA in a cell. The present RNA sequence represents a human IKK-
CC gamma substrate sequence.

XX Sequence 17 BP; 3 A; 5 C; 7 G; 0 T; 2 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 11; Length 17;

Best Local Similarity 87.5%; Pred. No. 2e+04; Mismatches 2; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAGGACCCGCGCAGUC 16

DB 1 UAGGACCCGCGCAGUC 16

RESULT 9

ADL14399 ADL14399 standard; DNA; 19 BP.

AC ADL14399;

XX 20-MAY-2004 (first entry)

DE PCR primer used to amplify the UGT Y486D isoform SeqID 8.

XX drug metabolic ability; UGT; UDP-glucuronosyl transferase;

KW gene analysis; liver function; Crigler-Najjar syndrome type I;

KW Crigler-Najjar syndrome type II; Gilbert syndrome;

KW Dublin-Johnson syndrome; Rotor syndrome; PCR; primer; ss.

XX Synthetic.

OS WO2004016814-A1.

PN 26-FEB-2004.

PD 13-FEB-2003; 2003WO-JP001475.

XX 12-AUG-2002; 2002JP-00235029.

XX (UTNI-) UNIV JAPAN SEC SHIGA MED.

XX Sato H, Fujiyama Y, Yamamoto K;

PI WPI; 2004-203813/19.

DR Estimation of drug metabolic activity by analyzing mutations in

PT glucuronosyltransferase gene, useful in studying drug metabolism, gene

PT analysis and clinical examination e.g. of diseases.

XX Disclosure; SEQ ID NO 8; 33pp; Japanese.

XX This invention relates to a novel method for examining the drug metabolic

CC ability of UGT (UDP-glucuronosyl transferase). Specifically, it refers

CC to the use of nucleic acid chips and/or arrays with an appropriate

CC oligonucleotide probe to detect mutations existing in exon 5 of the UGT

CC gene. The present invention describes the method as useful for studying

CC drug metabolism, gene analysis and for the clinical examination of

CC diseases that are associated with abnormal liver function including

CC Crigler-Najjar syndrome types I and II, Gilbert syndrome, Dublin-Johnson

CC syndrome and Rotor syndrome. This oligonucleotide sequence is a PCR

CC primer used to amplify a UGT DNA isoform, given in an exemplification of

CC the invention.

XX Sequence 19 BP; 2 A; 5 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 12; Length 19;

Best Local Similarity 68.8%; Pred. No. 2e+04; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGACCCGCGCAGUC 18

DB 4 GGACCCGCGCAGUC 18

RESULT 10

AAF69353 AAF69353 standard; DNA; 20 BP.

XX AAF69353;

XX 18-APR-2001 (first entry)

DE Integrin-linked kinase 3'UTR targeted oligonucleotide #2.

KW Antisense; integrin-linked kinase; hIK; infection; tumour; inflammation;

KW ss.

OS Homo sapiens.

PN US6177273-B1.

PD 23-JAN-2001.

XX 26-OCT-1999; 99US-00428219.

XX 26-OCT-1999; 99US-00428219.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Cowse LM;

XX WPI; 2001-137069/14.

DR Novel antisense compounds capable of modulating expression of human

PT Integrin-linked kinase, useful for diagnosis, prophylaxis and treatment

PT of diseases, e.g. tumors, associated with expression of the kinase.

XX Claim 3; Col 45; 40pp; English.

XX The present invention relates to an antisense compound 8 to 30 bases in

CC length targeted to the 5' untranslated (UTR) region, the coding region or

CC the 3' UTR region human Integrin-linked kinase (hIK). The antisense

CC oligonucleotides are useful for inhibiting the expression of human hIK in

CC human cells or tissues, in vitro. The oligonucleotides can be utilized

CC for diagnostics, therapeutics for the treatment of diseases associated

CC with the expression of hIK, prophylaxis e.g. to prevent or delay

CC infection, inflammation or tumor formation and as research reagent

XX Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 4; Length 20;

Best Local Similarity 68.8%; Pred. No. 2e+04; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGGACCCGCGCAGUC 17

DB 3 AGGACCCGCGCAGUC 17

ADBE43705/C

ID ADB43705 standard; DNA; 20 BP.

XX ADB43705;

XX 29-JAN-2004 (first entry)

XX Human KNSL1 sequencing primer, SEQ ID 310.

DE Neurodegenerative disease; uPA; SNGC; IDE; KNSL1; LIPA; TNFRSF6;

KW Alzheimer's disease; neuroprotective; nootropic; gene therapy;

KW Chromosome 10; PCR; primer; ss.

OS Homo sapiens.

OS WO2003054143-A2.

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XX 03-JUL-2003.
PD 25-OCT-2002; 2002WO-US034679.
XX
XX PF
XX 25-OCT-2001; 2001US-0339525P.
PR 08-NOV-2001; 2001US-0336929P.
PR 09-NOV-2001; 2001US-0338010P.
PR 04-DEC-2001; 2001US-0337052P.
PR 28-MAR-2002; 2002US-0368919P.
XX
XX (NEUR-) NEUROGENETICS INC.
PA (GEHO ) GEN HOSPITAL CORP.
XX
XX PI Becker KD, Velicelbi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;
XX WPI; 2003-559131/52.
XX
XX Determining a predisposition for or the occurrence of neurodegenerative
PT disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
PT the presence or absence of an allelic variant of one or more polymorphic
PT regions.
XX
XX Example 3; Page 291; 848pp; English.
XX
XX The present invention relates to a method (M1) for determining a
CC predisposition for or the occurrence of neurodegenerative disease in a
CC subject. The method comprises detecting in a target nucleic acid obtained
CC from the subject the presence or absence of an allelic variant of one or
CC more polymorphic regions of one or more genes selected from uPA
CC (urokinase plasminogen activator), SNOG (gamma-synuclein), IDE (insulin-
CC degrading enzyme), KNSL1 (kinesin-like protein 1), LIPA (lysosomal acid
CC lyase), and TNFRSF6 (Tumour Necrosis Factor Receptor-Sf6), where the
CC presence of at least one of the allelic variant of one or more
CC polymorphic regions is indicative of a predisposition for or the
CC occurrence of neurodegenerative disease. The genes are all located on
CC chromosome 10. M1 is useful for determining a predisposition for or the
CC occurrence of, and for treating neurodegenerative disease, particularly
CC Alzheimer's disease. The present sequence is a PCR primer, which was used
CC in the method of the invention.
XX
XX Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
SQ
Query Match 61.0%; Score 12.8; DB 10; Length 20;
Best Local Similarity 68.8%; Pred. No. 2e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 1 UAGACCGUGCCAGUC 16
DB 16 TAGGCTCGCTCCTTC 1
RESULT 12
ADL25330
ID ADL25330 standard; DNA; 20 BP.
XX
XX ADL25330;
AC
XX 20-MAY-2004 (first entry)
XX
XX Intestinal epithelium/peyer's patch M cell-associated PCR primer #475.
XX
XX Intestinal epithelium cell development; peyer's patch M cell development;
XX inflammatory bowel disease; glutenenteropathy; infectious disease;
XX autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
XX Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;
XX immune system disorder; hypersensitivity; anaphylaxis;
XX blood group incompatibility; ss; PCR; primer.
XX
XX Macaca fascicularis.
XX
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PN WO200280852-A2.
XX
XX PD 17-OCT-2002.
XX
XX PF 04-APR-2002; 2002WO-US010873.
XX
XX PR 04-APR-2001; 2001US-0281416P.
XX
XX PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
XX Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;
XX WPI; 2003-075470/07.
XX
XX Novel isolated or purified polypeptide encoded by genes associated with
PT intestinal epithelium or M cell development, differentiation or function,
PT useful for treating autoimmune diseases and infectious diseases.
XX
XX Disclosure; SEQ ID NO 840; 152pp; English.
XX
XX The invention comprises DNA sequences which are associated with
CC intestinal epithelium and peyer's patch M cells. The DNA sequences of the
CC invention are useful for assessing, modifying, modulating or regulating
CC intestinal epithelium or M cell development. The DNA sequences of the
CC invention are also useful in the treatment of: inflammatory bowel
CC disease, glutenenteropathy, infectious diseases, autoimmune diseases
CC (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's
CC disease, multiple sclerosis, allergy, asthma and diabetic mellitus),
CC diseases or disorders of the immune system, hypersensitivity,
CC anaphylaxis, and blood group incompatibility. The present DNA sequence
CC represents a PCR primer that was used to amplify an intestinal
CC epithelium/peyer's patch M cell-associated DNA sequence of the invention.
XX
XX Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
SQ
Query Match 61.0%; Score 12.8; DB 10; Length 20;
Best Local Similarity 62.5%; Pred. No. 2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 6 CCUGCCGAGUCUCUUTT 21
DB 4 CCTGCGATTGCTCCTT 19
RESULT 13
ADH54183/c
ID ADH54183 standard; DNA; 20 BP.
XX
XX ADH54183;
AC
XX 25-MAR-2004 (first entry)
XX
XX Human neurodegenerative disease-related sequencing primer SeqID3310.
XX
XX human; neurodegenerative disease; urokinase plasminogen activator; uPA;
XX gamma-synuclein; SNOG; insulin degrading enzyme; IDE;
XX kinesin-like protein 1; KNSL1; lysosomal acid lyase; LIPA;
XX tumour necrosis factor receptor Sf6; TNFRSF6; Alzheimer's disease; PCR;
XX primer; ss; sequencing.
XX
XX Homo sapiens.
XX
XX US2003224380-A1.
XX
XX 04-DEC-2003.
XX
XX 25-OCT-2002; 2002US-00282174.
XX
XX 25-OCT-2001; 2001US-0339525P.
XX
XX 25-OCT-2001; 2001US-0348065P.
XX
XX 02-NOV-2001; 2001US-0336983P.
XX
XX 08-NOV-2001; 2001US-0336929P.
XX
XX 08-NOV-2001; 2001US-0338010P.
XX
```


PT	mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT	cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX	
XX	Claim 4; SEQ ID NO 1205; 985bp; English.
PS	
CC	The invention comprises an antisense oligonucleotides that are targeted
CC	to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC	antisense oligonucleotides of the invention are useful for preventing or
CC	delaying infection, inflammation or tumor formation. The antisense
CC	oligonucleotides are also useful for treating diabetes, obesity,
CC	cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC	present DNA sequence represents an antisense oligonucleotide that targets
CC	the human glucocorticoid receptor gene. NOTE: The present sequence
CC	contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX	
SQ	Sequence 20 BP, 3 A, 7 C, 2 G, 8 T, 0 U, 0 Other;
Query Match	61.0%; Score 12.8; DB 12; Length 20;
Best Local Similarity	62.0%; Pred. NO. 2e+04;
Matches	10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY	6 CCUGCCAGUGCUCUUTT 21
: : :	
Db	1 CCTTCACATGCTCTTT 16
RESULT 15	
ADH63823	
ID	ADH63823 standard; DNA, 20 BP.
XX	
NC	ADH63823;

DT	25-MAR-2004 (first entry)
XX	
DE	Human glucocorticoid receptor-specific antisense oligonucleotide #657.
XX	
KW	antisense oligonucleotide; glucocorticoid receptor; infection;
KM	inflammation; tumor formation; diabetes; obesity;
KM	cardiovascular disorder; hyperlipidaemia; Cushing's
KM	phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX	
OS	Homo sapiens.
PN	WO2003099215-A2.
XX	
PD	04-DEC-2003.
XX	
PF	20-MAY-2003; 2003WO-US016084.
XX	
PR	20-MAY-2002; 2002US-0381857P.
XX	
PA	(PHAA) PHARMACIA CORP.
XX	
P1	Crosby SD, Naiseth AE;
DR	WPI; 2004-035034/03.
XX	
PT	New antisense compound targeted to a nucleic acid molecule encoding
PT	mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT	cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX	
PS	Claim 4; SEQ ID NO 657; 985bp; English.
XX	
CC	The invention comprises an antisense oligonucleotides that are targeted
CC	to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC	antisense oligonucleotides of the invention are useful for preventing or
CC	delaying infection, inflammation or tumor formation. The antisense
CC	oligonucleotides are also useful for treating diabetes, obesity,
CC	cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC	present DNA sequence represents an antisense oligonucleotide that targets
CC	the human glucocorticoid receptor gene. NOTE: The present sequence
CC	contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX	

Seq Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
 Query Match 61.0%; Score 12.8; DB 12; Length 20;
 Best Local Similarity 62.5%; Pred.No. 2e+04; 2;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 6 CCUGCCAGUGCUCUTT 21
 ||: ||| : ||: |||
 Db 2 CCTCCACGCTCTTT 17

Search completed: September 17, 2005, 10:22:12
 Job time : 266 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 09:50:06 ; Search time 1907 Seconds
(without alignments)
419.166 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 uagagccugccagcugcucnt 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 15386

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_hic: *
4: gb_esc3: *
5: gb_esc4: *
6: gb_esc5: *
7: gb_esc6: *
8: gb_g881: *
9: gb_g882: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	12.4	59.0	20	8	AZ496283	1M0332D09
2	11.4	54.3	19	8	AZ482658	AZ482658 1M0307L16
3	10.2	48.6	20	8	AZ398062	1M0163M14
4	10	47.6	20	7	CF337542	CF337542 JMT--08-A
5	9.8	46.7	19	8	AZ848554	AZ848554 2M0149A07
6	9.8	46.7	19	8	AZ868070	AZ868070 2M0179107
7	9.6	45.7	18	1	A1042533	A1042533 cy06e03.x
8	9.6	45.7	21	8	AZ656028	AZ656028 1M0531017
9	9.4	44.8	11	5	BQ592717	BQ592717 E012124-0
10	9.4	44.8	19	8	AZ772446	AZ772446 1M0583016
11	9.4	44.8	20	8	AZ625776	AZ625776 1M0465C08
12	9.2	43.8	16	9	CL657853	CL657853 PRI012C H
13	9.2	43.8	20	8	AZ827759	AZ827759 2M0104E22
14	9.2	43.8	20	8	AJ591869	AJ591869 Arabidops
15	9.2	43.8	21	8	AZ661719	AZ661719 1M0540M24
16	9.2	43.8	19	8	AZ514386	AZ514386 1M0361H02
17	9.2	43.8	19	8	AZ995149	AZ995149 2M0280D22
18	9.2	43.8	21	8	AZ304924	AZ304924 1M0005E05
19	9.2	43.8	21	8	AZ771145	AZ771145 1M0573A09
20	9.2	43.8	20	1	AJ747389	AJ747389 AJ747389
21	9.2	43.8	20	1	AJ747686	AJ747686 AJ747686
22	9.2	43.8	20	7	COT94844	COT94844 NT144D B0
23	9.2	43.8	20	8	AZ452238	AZ452238 1M0252C05
24	9.2	43.8	20	8	AZ503903	AZ503903 1M0343D24

C 25	8.8	41.9	20	8	AZ833768	AZ833768 2M0116002
C 26	8.8	41.9	21	1	AJ747329	AJ747329 AJ747329
C 27	8.8	41.9	21	4	BM398777	BM398777 5009-0-5-
C 28	8.8	41.9	21	8	AZ342282	AZ342282 1M0075H14
C 29	8.8	41.9	21	8	AZ581771	AZ581771 1M0370P10
C 30	8.6	41.0	17	7	CF310268	CF310268 ABF--04-N
C 31	8.6	41.0	18	8	AQ026356	AQ026356 1(3) rG554
C 32	8.6	41.0	19	7	CF307006	CF307006 HDAl--06-
C 33	8.6	41.0	19	7	CF307304	CF307304 HDAl--06-
C 34	8.6	41.0	19	7	CF307439	CF307439 HDAl--06-
C 35	8.6	41.0	19	8	AZ839439	AZ839439 2M0135L06
C 36	8.6	41.0	20	1	AJ652453	AJ652453 AJ652453
C 37	8.6	41.0	20	7	CF307027	CF307027 HDAl--05-
C 38	8.6	41.0	20	7	CF307258	CF307258 HDAl--06-
C 39	8.6	41.0	20	8	AZ946089	AZ946089 2M0207A13
C 40	8.6	41.0	20	8	AG202281	AG202281 Pan trog1
C 41	8.6	41.0	21	7	CF307437	CF307437 HDAl--06-
C 42	8.6	41.0	21	8	AZ862876	AZ862876 2M0170B18
C 43	8.6	41.0	21	9	AG196285	AG196285 Pan trog1
C 44	8.6	41.0	21	9	AG202462	AG202462 Pan trog1
C 45	8.6	41.0	21	9	AJ587178	AJ587178 Arabidops

ALIGNMENTS

RESULT 1
LOCUS AZ496283
DEFINITION 1M0332D09R Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM0332D09 R, genomic survey sequence.
ACCESSION AZ496283
VERSION AZ496283.1 GI:10672347
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Isiam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0332 row: D column: 09
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0332D09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 59.0%; Score 12.4; DB 8; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.9e+05;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 CUGCCAGUCUCUT 20
| | | | | : | | | | |
Db 1 CAGCCAGTCTCTT 14

RESULT 2

AZ482658/c 19 bp DNA linear GSS 05-OCT-2000
LOCUS 1M030716R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M030716 R, genomic survey sequence.
ACCESSION AZ482658
VERSION AZ482658.1 GI:10645919
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0307 row: L column: 16
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. 19

FEATURES
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/mol_type="genomic DNA"
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/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 54.3%; Score 11.4; DB 8; Length 19;
Best Local Similarity 76.9%; Pred. No. 8.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACCUGCCAGUCGU 17
| | | | | : | | | | |
Db 13 ACCTGCCAGAGCT 1

RESULT 3

A2398062/c 20 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0163M14F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0163M14 F, genomic survey sequence.
ACCESSION A2398062
VERSION A2398062.1 GI:10513134
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0163 row: M column: 14
Seq primer: CGTTGTAAGACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20

FEATURES
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/strain="C57BL/6J"
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/clone="UGCG1M0163M14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 48.6%; Score 10.2; DB 8; Length 20;
Best Local Similarity 60.0%; Pred. No. 3.4e+06;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGACUCCGACGUCU 17
|||:|||||:
Db 19 GGCCCTGCTGCT 5

RESULT 4
LOCUS CF337542 20 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--08-A10.b1 AtUMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--08-A10, mRNA sequence.
CF337542 GI:33823470

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
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/organism="Oryza sativa (japonica cultivar-group)"
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/clone_lib="AtUMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: PCR4-TOP0, Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis thaliana jasmonic acid Carboxyl methyltransferase overexpression line."

ORIGIN

Query Match 47.6%; Score 10; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.2e+06;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGACUCCGACGUCU 20
|||:|||||:
Db 2 GGTCATGACAGTGT 19

RESULT 5
LOCUS AZ848554 19 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0149A07R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUCG2M0149A07 R, genomic survey sequence.
AZ848554
AZ848554.1 GI:13031758

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Moyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0149 row: A column: 07
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0149A07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 46.7%; Score 9.8; DB 8; Length 19;
Best Local Similarity 53.8%; Pred. No. 5.2e+06;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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 Db 3 CTGCTAGTCTGT 15

RESULT 6
 A2868070 19 bp DNA linear GSS 21-FEB-2001
 LOCUS A1042533/c
 DEFINITION 2M0179107F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGCM0179107 F, genomic survey sequence.

ACCESSION A2868070
 VERSION A2868070.1 GI:13071017
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0179 row: I column: 07
 Seq primer: CGTGTAAACGACGCGCAGT
 Classes: Plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES
 source 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGCM0179107"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g1|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 46.7%; Score 9.8; DB 8; Length 19;
 Best Local Similarity 53.8%; Pred. No. 5.2e+06;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 CUGCCAGUGUCUCU 19
 ||:||||:|
 Db 15 CTGCTAGTCTGT 3

RESULT 7
 A1042533 18 bp mRNA linear EST 30-JUN-1998
 LOCUS A1042533/c
 DEFINITION cy60603.x1 Soares senescent fibroblasts NBHSF Homo sapiens cDNA
 clone IMAGE:1665052.3 similar to TR:Q15662 Q15662
 TRANSFORMATION-RELATED PROTEIN ; mRNA sequence.

ACCESSION A1042533
 VERSION A1042533.1 GI:3281727
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 18)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 trace considered overall poor quality
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 source 1..18
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1665052"
 /clease_type="senescent_fibroblast"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares senescent_fibroblasts_NBHSF"
 /note="Vector: pT7T3D (Pharmacia) with a modified
 polylinker V-type: phagemid; Site 1: Not I; Site 2: Eco
 RI; 1st strand cDNA was primed with a Not I - oligo (dT)
 primer [5',
 TGTATCAATCTGAAGAGGAGGCGCATTTTCTTTTCTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 45.7%; Score 9.6; DB 1; Length 18;
 Best Local Similarity 56.2%; Pred. No. 6.5e+06;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 CCUGCCAGUGUCUCU 21
 ||:||||:|
 Db 17 CTTTCAGTGTCA 2

RESULT 8
 A2656028 21 bp DNA linear GSS 14-DEC-2000
 LOCUS A2656028
 DEFINITION IM0531017F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGIM0531017 F, genomic survey sequence.

ACCESSION A2656028
 VERSION A2656028.1 GI:11793174
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0179 row: I column: 07
 Seq primer: CGTGTAAACGACGCGCAGT
 Classes: Plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0531 row: 0 column: 17
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0531017"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gt|4732114|gb|AF19072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 45.7%; Score 9.6; DB 8; Length 21;
Beet Local Similarity 50.0%; Pred. No. 6.6e+06;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 6 CCUGCCAGUCUCUUTT 21
DB 5 CCTACAGTGCCTTAT 20

RESULT 9
BO592717/c 11 bp mRNA linear EST 06-DEC-2002
LOCUS E012124-024-028-J16-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
DEFINITION cDNA clone 024-028-J16 5-PRIME, mRNA sequence.
ACCESSION BO592717.1 GI:26122300
VERSION BO592717.1
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (bases 1 to 11)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigenes' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp1z-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 28 row: 1 column: 16
Seq primer: SP6; CATACGATTGATGACACTATAG.
Location/Qualifiers
1. .11
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:194137"
/db_xref="taxon:161934"
/clone="024-028-J16"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinzehnleberer Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZP/GABI-Primary database: http://gabi.rzp.de"

ORIGIN
Query Match 44.8%; Score 9.4; DB 5; Length 11;
Beet Local Similarity 72.7%; Pred. No. 7.6e+06;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 5 ACCUGCCAGUG 15
DB 11 ACCTACGAGTG 1

RESULT 10
A2772446 19 bp DNA linear GSS 16-FEB-2001
LOCUS I00583016f Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0583016 F, genomic survey sequence.
ACCESSION A2772446
VERSION A2772446
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0583 row: 0 column: 16
Seq primer: CGTGTGTAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0583016"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 44.8%; Score 9.4; DB 8; Length 19;
Best Local Similarity 72.7%; Pred. No. 8.2e+06;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 5 ACCUGCCAGUG 15
|||:|||||
6 ACCTGACAGTG 16

RESULT 11
A2625776 20 bp DNA linear GSS 13-DEC-2000
LOCUS A2625776.1
DEFINITION 1M0465C08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0465C08 R, genomic survey sequence.
ACCESSION A2625776
VERSION A2625776.1 GI:11747966
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Mennen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0465 row: C column: 08
Seq primer: CACACAGGAAACACTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0465C08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 44.8%; Score 9.4; DB 8; Length 20;
Best Local Similarity 47.4%; Pred. No. 8.2e+06;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Qy 1 UAGGACCGCCAGUGUCUCU 19
:|||||:|||||:
19 TAGAATCTTGAGAGCGCCT 1

RESULT 12
CL657853 16 bp DNA linear GSS 09-JUN-2004
LOCUS CL657853
DEFINITION PR1012C_H07 - PR1012C.B21 (16) Mixed stage foetid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL657853
VERSION CL657853.1 GI:50139888
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 16)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
Appads: an Acce database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
CONTACT: Sommer RJ
JOURNAL Evolutionary Biology

Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7

Class: fosmid ends.

FEATURES

Source
1..16
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pBplfos-5 Fosmid vector"

ORIGIN

Query Match 43.8%; Score 9.2; DB 9; Length 16;
Best Local Similarity 50.0%; Pred. No. 1e+07;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 8 UGCCAGUCGUCUTT 21
:||||:|:|:
Db 3 TACCACTACTCTCT 16

RESULT 13
AZ827759/c 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0104222F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0104E22 F, genomic survey sequence.
ACCESSION AZ827759
VERSION AZ827759.1 GI:12997667
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Jellum, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0104 row: E column: 22
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20

FEATURES

Source
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC2M0104E22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gblAF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 43.8%; Score 9.2; DB 8; Length 20;
Best Local Similarity 57.1%; Pred. No. 1e+07;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 UGCCAGUCGUCUTT 21
:||||:|:|:
Db 20 TCCAGTGCAGT 7

RESULT 14
AJ591869/c 20 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
594C10, genomic survey sequence.
ACCESSION AJ591869
VERSION AJ591869.1 GI:37941493
KEYWORDS GSS: left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samsen, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepoint, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
12446565
2 (bases 1 to 20)
Balzerque, S.
Direct Submission
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment (b) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

FEATURES

Source
1..20
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Masilllewska"
/db_xref="taxon:3702"

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/c/clone="594C10"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/misc_feature 1..20 "T-DNA flanking sequence
             /note="T-DNA flanking sequence
             left border"

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ORIGIN

```

Query Match      43.8%; Score 9.2; DB 9; Length 20;
Best Local Similarity 71.4%; Pred. No. 1e+07;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Oy      5 ACCUGCCAGUGCUC 18
        |||||:||||
        17 ACTAGCCAGTGCAC 4

```

RESULT 15

```

A2661719      21 bp DNA linear GSS 14-DEC-2000
LOCUS      1M0540M24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION  clone UUGC1M0540M24 F, genomic survey sequence.
ACCESSION  A2661719
VERSION    A2661719.1 GI:11798865
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

```

```

REFERENCE
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 21)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Isiam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.

```

TITLE

```

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

```

JOURNAL

```

COMMENT      Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std. Error: 0.00
            Plate: 0540 row: M column: 24
            Seq primer: CGTGTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
            Location/Qualifiers

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FEATURES

SOURCE

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1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0540M24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

```

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

```

Query Match      43.8%; Score 9.2; DB 8; Length 21;
Best Local Similarity 64.3%; Pred. No. 1e+07;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Oy      2 AGGACCGCCAGUG 15
        |||||:||||
        Db      5 AGGACGTGTAGTG 18

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Search completed: September 17, 2005, 11:19:51
Job time : 1914 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 07:53:35; Search time 94 Seconds
(without alignments)
365.551 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 uagaccugccagugcucut 21

Scoring table: IDENTITY_NUC

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 457068

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.8	61.0	20	3	US-09-428-219-82
2	12.4	59.0	17	3	US-08-998-099-62
3	12.4	59.0	20	4	US-09-198-452A-6154
4	12.2	58.1	20	4	US-09-861-158-78
5	12.2	57.1	21	1	US-07-937-609-5
6	12.2	57.1	21	1	US-08-029-170-5
7	12.2	57.1	21	4	US-09-443-745-5
8	12.2	57.1	21	4	US-09-657-472-877
9	11.8	56.2	20	3	US-09-702-327-53
10	11.8	56.2	20	3	US-09-517-467B-256
11	11.8	56.2	20	4	US-09-657-346A-69
12	11.8	56.2	20	4	US-09-900-920-12
13	11.8	56.2	21	4	US-09-657-472-1359
14	11.6	55.2	20	2	US-08-117-952-361
15	11.6	55.2	20	3	US-09-313-933-485
16	11.6	55.2	20	3	US-09-517-467B-337
17	11.6	55.2	20	4	US-09-198-452A-2895
18	11.4	54.3	17	1	US-08-152-313-113
19	11.4	54.3	17	1	US-08-579-223-113
20	11.4	54.3	17	4	US-09-474-433B-479
21	11.4	54.3	17	4	US-09-474-433B-859
22	11.4	54.3	17	4	US-09-476-387-478
23	11.4	54.3	17	4	US-09-476-387-858
24	11.4	54.3	17	5	PCT-US94-12947A-113
25	11.4	54.3	18	3	US-08-257-963B-35
26	11.4	54.3	18	3	US-08-367-841A-35
27	11.4	54.3	18	5	PCT-US95-07201-35

c	28	11.4	54.3	20	3	US-09-428-583-44	Sequence 44, Appl
c	29	11.4	54.3	20	3	US-09-844-634-57	Sequence 57, Appl
c	30	11.4	54.3	20	4	US-09-657-346A-40	Sequence 40, Appl
c	31	11.4	54.3	20	4	US-09-608-958-5	Sequence 5, Appl
c	32	11.4	54.3	20	4	US-09-422-978-5960	Sequence 5960, Ap
c	33	11.4	54.3	21	1	US-08-240-547-42	Sequence 42, Appl
c	34	11.2	53.3	17	2	US-08-292-620A-1886	Sequence 1886, Ap
c	35	11.2	53.3	17	2	US-08-292-620A-1977	Sequence 1977, Ap
c	36	11.2	53.3	17	3	US-09-071-845-1886	Sequence 1886, Ap
c	37	11.2	53.3	17	3	US-09-071-845-1977	Sequence 1977, Ap
c	38	11.2	53.3	19	3	US-09-522-800-11	Sequence 11, Appl
c	39	11.2	53.3	20	4	US-09-198-452A-6127	Sequence 6127, Ap
c	40	11.2	53.3	21	4	US-09-366-257-2	Sequence 2, Appl
c	41	11.2	53.3	21	4	US-09-422-978-11690	Sequence 11690, A
c	42	11.2	53.3	21	4	US-09-889-732-2	Sequence 2, Appl
c	43	11.2	53.3	21	4	US-08-278-774-29	Sequence 29, Appl
c	44	11.2	52.4	19	3	US-09-407-818-11	Sequence 11, Appl
c	45	11.2	52.4	19	4	US-09-696-791-1998	Sequence 1998, Ap

ALIGNMENTS

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RESULT 1
US-09-428-219-82
; Sequence 82, Application US/09428219
; Patent No. 6177273
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN-LINKED KINASE EXPRESSION
; FILE REFERENCE: RUS-0101
; CURRENT APPLICATION NUMBER: US/09/428,219
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-219-82

Query Match      61.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 68.8%; Pred. No. 5.5e+03;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy      2 AGGACCGCAGUCU 17
Db      3 AGGACCTTCAGTCT 18

RESULT 2
US-08-998-099-62/c
; Sequence 62, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGEN, JAMES A.
; APPLICANT: STINCHCOMB, DAN T.
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; CURRENT FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/773,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; EARLIER FILING DATE: 1994-05-18
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSeq for Windows Version 3.0
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SEQ ID NO 62
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-08-998-099-62

Query Match
Best Local Similarity 59.0%; Score 12.4; DB 3; Length 17;
Best Local Similarity 64.3%; Pred. No. 8.4e+03;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCUGCCAGUCUCU 19
DB 15 CCGCCAGTCTCT 2

RESULT 3
US-09-198-452A-6154/C
Sequence 6154, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffeis, R
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 6154
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6154

Query Match
Best Local Similarity 59.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 64.3%; Pred. No. 8.6e+03;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 8 UGCGAGUCUCU 21
DB 15 TCGCTGTCTCTT 2

RESULT 4
US-09-861-159-78/C
Sequence 78, Application US/09861159
Patent No. 6485974
GENERAL INFORMATION:
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF PTPN2 EXPRESSION
FILE REFERENCE: RTS-0243
CURRENT APPLICATION NUMBER: US/09/861,159
CURRENT FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 78
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-861-159-78

Query Match
Best Local Similarity 58.1%; Score 12.2; DB 4; Length 20;
Best Local Similarity 58.8%; Pred. No. 1.1e+04;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAGGACUGCCAGUCU 17
DB 20 TAGTACTGACAGTCT 4

RESULT 5

US-07-937-609-5/C
Sequence 5, Application US/07937609
Patent No. 5319073
GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/937,609
FILING DATE: 19920902
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-937-609-5

Query Match
Best Local Similarity 57.1%; Score 12; DB 1; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.4e+04;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGCCAGUCUC 18
DB 16 CTGCCAGTCTC 5

RESULT 6
US-08-029-170-5/C
Sequence 5, Application US/08029170
Patent No. 6169173
GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA

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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/029,170
FILING DATE: 19930310
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIND
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-08-029-170-5

Query Match      57.1%; Score 12; DB 3; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.4e+04;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 CUGCCAGUGCUC 18
DB      16 CTGCCAGTGTCTC 5

RESULT 7
US-09-443-745-5/C
Sequence 5, Application US/09443745
Patent No. 6706493
GENERAL INFORMATION:
APPLICANT: MANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECTOSTOMININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/443,745
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/029,170
FILING DATE: 10-MAR-1993
APPLICATION NUMBER: US 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIND
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-443-745-5

Query Match      57.1%; Score 12; DB 4; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.4e+04;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 CUGCCAGUGCUC 18
DB      16 CTGCCAGTGTCTC 5

RESULT 8
US-09-657-472-877
Sequence 877, Application US/09657472
Patent No. 6727063
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Daley, George O.
APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/225,724
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 877
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-09-657-472-877

Query Match      57.1%; Score 12; DB 4; Length 21;
Best Local Similarity 64.3%; Pred. No. 1.4e+04;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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Db 1 CCTGCCAGTGYCCT 14

RESULT 9

US-09-702-327-53

Sequence 53, Application US/09702327

Patent No. 6426220

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Lex M. Cowart

TITLE OF INVENTION: ANTISENSE MODULATION OF CALRETICULIN EXPRESSION

FILE REFERENCE: RTS-0097

CURRENT APPLICATION NUMBER: US/09/702,327

CURRENT FILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 89

SEQ ID NO 53

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-702-327-53

Query Match 56.2%; Score 11.8; DB 3; Length 20;

Best Local Similarity 73.3%; Pred. No. 1.7e+04;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACCCGCCAGUCUC 18

Db 5 GACCTGCCAGAGGTC 19

RESULT 10

US-09-517-467B-256/C

Sequence 256, Application US/09517467B

Patent No. 6451602

GENERAL INFORMATION:

APPLICANT: Ian Popoff

APPLICANT: Lex M. Cowart

TITLE OF INVENTION: ANTISENSE MODULATION OF PARP EXPRESSION

FILE REFERENCE: RTS-0150

CURRENT APPLICATION NUMBER: US/09/517,467B

CURRENT FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 09/517,467

PRIOR FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 345

SEQ ID NO 256

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-517-467B-256

Query Match 56.2%; Score 11.8; DB 3; Length 20;

Best Local Similarity 73.3%; Pred. No. 1.7e+04;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 URGACCTGCCAGUG 15

Db 19 TAGGACCGCAAGTG 5

RESULT 11

US-09-657-346A-69

Sequence 69, Application US/09657346A

Patent No. 6503754

GENERAL INFORMATION:

APPLICANT: Hong Zhang

APPLICANT: Jacqueline Wyatt

TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST

FILE REFERENCE: RTS-0135

CURRENT APPLICATION NUMBER: US/09/657,346A

CURRENT FILING DATE: 2000-09-07

NUMBER OF SEQ ID NOS: 174

SEQ ID NO 69

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-657-346A-69

Query Match 56.2%; Score 11.8; DB 4; Length 20;

Best Local Similarity 73.3%; Pred. No. 1.7e+04;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACCCGCCAGUCUC 18

Db 4 GACATGCCAGGCTC 18

RESULT 12

US-09-900-920-12/C

Sequence 12, Application US/09900920

Patent No. 6696562

GENERAL INFORMATION:

APPLICANT: Schultz-Cherry, Stacey

APPLICANT: Kelley, Laura

APPLICANT: Koci, Matthew

TITLE OF INVENTION: No. 6696562a1 Avian Astrovirus

FILE REFERENCE: turkeyastrovirus

CURRENT APPLICATION NUMBER: US/09/900,920

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,312

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 12

LENGTH: 20

TYPE: DNA

ORGANISM: Turkey Astrovirus

US-09-900-920-12

Query Match 56.2%; Score 11.8; DB 4; Length 20;

Best Local Similarity 66.7%; Pred. No. 1.7e+04;

Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 CUGCCAGUCUCUUTT 21

Db 17 CTGCCAGTGGTCATT 3

RESULT 13

US-09-657-472-1359/C

Sequence 1359, Application US/09657472

Patent No. 6727063

GENERAL INFORMATION:

APPLICANT: Lander, Eric S.

APPLICANT: Cargill, Michele

APPLICANT: Ireland, James S.

APPLICANT: Bolik, Stacey

APPLICANT: Daley, George O.

APPLICANT: McCarthy, Jeanette J.

TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES

FILE REFERENCE: 2825.1027-001

CURRENT APPLICATION NUMBER: US/09/657,472

CURRENT FILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: US 60/153,357

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US 60/220,947

PRIOR FILING DATE: 2000-07-26

PRIOR APPLICATION NUMBER: US 60/225,724

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1359
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-09-657-472-1359

Query Match
Best Local Similarity 64.7%; Score 11.8; DB 4; Length 21;
Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AGGACCGCCAGUCGUC 18
Db 18 AGGCTCTCCAGAGCTC 2

RESULT 14
US-08-117-952-361/c
Sequence 361, Application US/08117952
Patent No. 5851760
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
APPLICANT: Smith, Michael W.
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9423
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 361:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Oligonucleotide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-117-952-361

Query Match
Best Local Similarity 55.2%; Score 11.6; DB 2; Length 20;
Pred. No. 2.1e+04;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GACCGCCAGUCGUCUTT 21
Db 18 GGCTCTGCGAGTGTATTT 1

RESULT 15
US-09-313-932-485/c
Sequence 485, Application US/09313932A
Patent No. 6228642
GENERAL INFORMATION:
APPLICANT: Baker, Brenda
APPLICANT: Bennett, C. Frank
APPLICANT: Butler, Madeline M.
APPLICANT: Shanahan, William R.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: ISPH-0356
CURRENT APPLICATION NUMBER: US/09/313,932A
CURRENT FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 501
SEQ ID NO 485
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-313-932-485

Query Match
Best Local Similarity 55.2%; Score 11.6; DB 3; Length 20;
Pred. No. 2.1e+04;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 UAGGACCGCCAGUCGUC 18
Db 18 TAGGAGCTGCGCTGAGCTC 1

Search completed: September 17, 2005, 09:08:20
Job time : 96 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 08:31:40 : Search time 390 Seconds
(without alignments)
358.754 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 usgaccgcccagugcucut 21

Scoring table: IDENTITY_NUC

Searched: 7389322 seqs, 3331285599 residues

Total number of hits satisfying chosen parameters: 2069766

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10I_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	US-10-738-413-1	Sequence 1, Appl
2	18	85.7	20	US-10-424-041-41	Sequence 41, Appl
3	18	85.7	20	US-10-424-041-132	Sequence 132, Appl
4	17	81.0	20	US-10-424-041-56	Sequence 56, Appl
5	17	81.0	20	US-10-424-041-144	Sequence 144, Appl
6	13.6	64.8	20	US-10-304-082-11	Sequence 11, Appl
7	13.6	64.8	20	US-10-304-082-48	Sequence 48, Appl

8	13.6	64.8	21	US-10-847-918-2129	Sequence 2129, Ap
c 9	13.4	62.9	18	US-10-924-375-91	Sequence 91, Appl
10	13.2	63.8	20	US-11-039-629-89	Sequence 89, Appl
11	12.8	61.0	17	US-10-156-306-5959	Sequence 5959, Ap
12	12.8	61.0	17	US-10-156-306-7065	Sequence 7065, Ap
c 13	12.8	61.0	20	US-10-282-174-310	Sequence 310, Appl
c 14	12.8	61.0	20	US-10-188-883-82	Sequence 82, Appl
c 15	12.8	61.0	20	US-10-671-395-720	Sequence 720, Appl
c 16	12.8	61.0	20	US-10-671-395-995	Sequence 995, Appl
c 17	12.8	61.0	20	US-10-671-395-1209	Sequence 1209, Appl
c 18	12.8	61.0	20	US-10-671-395-1392	Sequence 1392, Appl
c 19	12.8	61.0	20	US-10-671-395-1473	Sequence 1473, Appl
c 20	12.8	61.0	20	US-10-600-009-310	Sequence 310, Appl
c 21	12.8	61.0	20	US-10-829-674-396	Sequence 396, Appl
22	12.8	61.0	20	US-10-830-477-396	Sequence 396, Appl
23	12.6	60.0	21	US-10-386-243-5	Sequence 5, Appl1
c 24	12.4	59.0	20	US-10-005-956-1172	Sequence 1172, Appl
c 25	12.4	59.0	20	US-10-289-762-6154	Sequence 6154, Appl
c 26	12.4	59.0	20	US-10-300-611-39	Sequence 39, Appl1
c 27	12.4	59.0	20	US-10-671-395-957	Sequence 957, Appl
c 28	12.4	59.0	20	US-10-671-395-1552	Sequence 1552, Appl
c 29	12.2	58.1	19	US-10-665-951-1599	Sequence 1599, Appl
c 30	12.2	58.1	19	US-10-665-951-1846	Sequence 1846, Appl
c 31	12.2	58.1	19	US-10-758-155-1599	Sequence 1599, Appl
c 32	12.2	58.1	19	US-10-758-155-1846	Sequence 1846, Appl
c 33	12.2	58.1	19	US-10-831-620-1599	Sequence 1599, Appl
c 34	12.2	58.1	19	US-10-831-620-1846	Sequence 1846, Appl
c 35	12.2	58.1	19	US-10-844-076-1599	Sequence 1599, Appl
c 36	12.2	58.1	20	US-10-844-076-1846	Sequence 1846, Appl
c 37	12.2	58.1	20	US-10-475-146-78	Sequence 78, Appl1
c 38	12.2	58.1	20	US-10-257-158A-6705	Sequence 6705, Appl
39	12.2	58.1	21	US-10-751-736-36179	Sequence 36179, A
c 40	12	57.1	17	US-09-818-875-1910	Sequence 1910, Appl
c 41	12	57.1	17	US-09-818-875-1911	Sequence 1911, Appl
c 42	12	57.1	17	US-09-818-875-1914	Sequence 1914, Appl
c 43	12	57.1	17	US-09-818-875-1915	Sequence 1915, Appl
c 44	12	57.1	17	US-10-209-787-1910	Sequence 1910, Appl
c 45	12	57.1	17	US-10-209-787-1911	Sequence 1911, Appl

ALIGNMENTS

RESULT 1
US-10-738-413-1
; Sequence 1, Application US/10738413
; Publication No. US20050137151A1
; GENERAL INFORMATION:
; APPLICANT: BINETTI, RALPH R.
; TITLE OF INVENTION: SI-RNA-MEDIATED GENE SILENCING TECHNOLOGY TO INHIBIT
; FILE REFERENCE: SC66U-US
; CURRENT FILING DATE: 2003-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic
; FEATURE:
; OTHER INFORMATION: oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-738-413-1

Query Match 100.0%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 UAGACCGCCAGGUCGUCU 21
|||
DB 1 UAGACCGCCAGGUCGUCU 21

RESULT 2

US-10-424-041-41/c
; Sequence 41, Application US/10424041
; Publication No. US20040215006A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
; FILE REFERENCE: BIOL000505
; CURRENT APPLICATION NUMBER: US/10/424,041
; CURRENT FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 184
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-424-041-41

Query Match 85.7%; Score 18; DB 20; Length 20;
Best Local Similarity 77.8%; Pred. No. 33;

Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 UAGACCGCCAGGUCGUC 18
:|||||:|||||:|
DB 18 TAGGACCTGCCAGTGCTC 1

RESULT 3

US-10-424-041-132
; Sequence 132, Application US/10424041
; Publication No. US20040215006A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
; FILE REFERENCE: BIOL000505
; CURRENT APPLICATION NUMBER: US/10/424,041
; CURRENT FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 184
; SEQ ID NO 132
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-424-041-132

Query Match 85.7%; Score 18; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 UAGACCGCCAGGUCGUC 18
|||||
DB 3 UAGACCGCCAGGUCGUC 20

RESULT 4

US-10-424-041-56/c
; Sequence 56, Application US/10424041
; Publication No. US20040215006A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon

; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
; FILE REFERENCE: BIOL000505
; CURRENT APPLICATION NUMBER: US/10/424,041
; CURRENT FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 184
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-424-041-56

Query Match 81.0%; Score 17; DB 20; Length 20;
Best Local Similarity 76.5%; Pred. No. 11e+02;

Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 UAGACCGCCAGGUCU 17
:|||||:|||||:|
DB 17 TAGGACCTGCCAGTGCT 1

RESULT 5

US-10-424-041-144
; Sequence 144, Application US/10424041
; Publication No. US20040215006A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
; FILE REFERENCE: BIOL000505
; CURRENT APPLICATION NUMBER: US/10/424,041
; CURRENT FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 184
; SEQ ID NO 144
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-424-041-144

Query Match 81.0%; Score 17; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 UAGACCGCCAGGUCU 17
|||||
DB 4 UAGACCGCCAGGUCU 20

RESULT 6

US-10-304-082-11
; Sequence 11, Application US/10304082
; Publication No. US20040102401A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
; FILE REFERENCE: PTS-0037
; CURRENT APPLICATION NUMBER: US/10/304,082
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-10-304-082-11

Query Match 64.8%; Score 13.6; DB 19; Length 20;
 Best Local Similarity 70.0%; Pred. No. 5.9e+03;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACUCCAGGUCUCU 21
 Db 1 AGGACUCCAGGUCUCU 20

RESULT 7

US-10-304-082-48/c
 ; Sequence 48, Application US/10304082
 ; Publication No. US20040102401A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas M. Dean
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
 ; FILE REFERENCE: PTS-0037
 ; CURRENT APPLICATION NUMBER: US/10/304,082
 ; CURRENT FILING DATE: 2002-11-22
 ; NUMBER OF SEQ ID NOS: 78
 ; SEQ ID NO 48
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: H. sapiens
 ; FEATURE:
 US-10-304-082-48

Query Match 64.8%; Score 13.6; DB 19; Length 20;
 Best Local Similarity 70.0%; Pred. No. 5.9e+03;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACUCCAGGUCUCU 21
 Db 20 AGGACUCCAGGUCUCU 1

RESULT 8

US-10-847-918-2129
 ; Sequence 2129, Application US/10847918
 ; Publication No. US20050119210A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Be, Xiaobing
 ; APPLICANT: Liu, Wei
 ; APPLICANT: Slonim, Donna
 ; APPLICANT: Howes, Steve
 ; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
 ; FILE REFERENCE: 031896-026000 (AM101264)
 ; CURRENT APPLICATION NUMBER: US/10/847,918
 ; CURRENT FILING DATE: 2004-05-19
 ; PRIOR APPLICATION NUMBER: US 60/471,729
 ; PRIOR FILING DATE: 2003-05-20
 ; NUMBER OF SEQ ID NOS: 14937
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2129
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: RNAI-sense strand
 US-10-847-918-2129

Query Match 64.8%; Score 13.6; DB 21; Length 21;
 Best Local Similarity 75.0%; Pred. No. 6e+03; 4; Indels 0; Gaps 0;
 Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 UAGAGCUGCCAGUCUCU 20
 Db 2 UCGAGCUGCCAGUCUCU 21

RESULT 9

US-10-924-375-91/c
 ; Sequence 91, Application US/10924375
 ; Publication No. US20050130190A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Antzelevitch, Charles
 ; APPLICANT: Brugada, Ramon
 ; APPLICANT: Hong, Kui
 ; TITLE OF INVENTION: Mutations in Ion Channel Proteins Associated with Sudden Cardiac
 ; FILE REFERENCE: 1396-2
 ; CURRENT APPLICATION NUMBER: US/10/924,375
 ; CURRENT FILING DATE: 2004-08-23
 ; PRIOR APPLICATION NUMBER: 60/497,256
 ; PRIOR FILING DATE: 1998-08-22
 ; NUMBER OF SEQ ID NOS: 134
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 91
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: primer
 US-10-924-375-91

Query Match 63.8%; Score 13.4; DB 22; Length 18;
 Best Local Similarity 66.7%; Pred. No. 7.5e+03;
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ACCUGCCAGUCUCU 19
 Db 16 ACCTGCCAGTCTGT 2

RESULT 10

US-11-039-629-89
 ; Sequence 89, Application US/11039629
 ; Publication No. US20050164271A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bhanot, Sanjay
 ; APPLICANT: Dobie, Kenneth W.
 ; APPLICANT: Freiler, Susan M.
 ; APPLICANT: Dean, Nicholas M.
 ; APPLICANT: Bennett, C. Frank
 ; TITLE OF INVENTION: MODULATION OF GLUCOCORTICOID RECEPTOR
 ; FILE REFERENCE: RTS-0532US
 ; CURRENT APPLICATION NUMBER: US/11/039,629
 ; CURRENT FILING DATE: 2005-01-20
 ; PRIOR APPLICATION NUMBER: 60/538,173
 ; PRIOR FILING DATE: 2004-01-20
 ; PRIOR APPLICATION NUMBER: 60/550,191
 ; PRIOR FILING DATE: 2004-03-03
 ; NUMBER OF SEQ ID NOS: 310
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 89
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Compound
 US-11-039-629-89

Query Match 62.9%; Score 13.2; DB 24; Length 20;
 Best Local Similarity 61.1%; Pred. No. 9.5e+03;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GACUCCAGGUCUCU 21
 Db 3 GTCTTCCAGTCTCTTT 20

RESULT 11

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US-10-156-306-5959
; Sequence 5959, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MGS19gen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5959
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-5959

Query Match      61.0%; Score 12.8; DB 15; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 UAGACCTGCGCCAGUGC 16
      |||||:|||||:|
Db      1 UAGGCGCGCGCCAGUGC 16

RESULT 12
US-10-156-306-7065
; Sequence 7065, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MGS19gen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7065
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-7065

Query Match      61.0%; Score 12.8; DB 15; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 UAGACCTGCGCCAGUGC 16
      |||||:|||||:|
Db      2 UAGGCGCGCGCCAGUGC 17

RESULT 13
US-10-282-174-310/c
; Sequence 310, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Vejicelcibi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertiam, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
```

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; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-282-174-310

Query Match      61.0%; Score 12.8; DB 17; Length 20;
Best Local Similarity 68.8%; Pred. No. 1.5e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 UAGACCTGCGCCAGUGC 16
      :|||:|:|:|:|
Db      16 TAGGTCTGCGCATTC 1

RESULT 14
US-10-188-883-82
; Sequence 82, Application US/10188883
; Publication No. US2004000605A1
; GENERAL INFORMATION:
; APPLICANT: Bhanot, Sanjay
; TITLE OF INVENTION: USE OF INTEGRIN-LINKED KINASE INHIBITORS FOR TREATING INSULIN RESI
; FILE REFERENCE: ISPH-0687
; CURRENT APPLICATION NUMBER: US/10/188,883
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide.
US-10-188-883-82

Query Match      61.0%; Score 12.8; DB 17; Length 20;
Best Local Similarity 68.8%; Pred. No. 1.5e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 AGGACCTGCGCCAGUGC 17
      |||||:|||||:|
Db      3 AGGACCTTCCAGTCT 18

RESULT 15
US-10-671-395-720/c
; Sequence 720, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
```

```

; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 720
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-720

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Query Match      61.0%; Score 12.8; DB 19; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      6 CCUGCCAGUCUCUUTT 21
      ||:|||||:|:|:|
Db      20 CCTGCCAGTCTCTGT 5

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Search completed: September 17, 2005, 10:17:43
 Job time : 393 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 08:00:46 ; Search time 2487 Seconds
(without alignments)
344.706 Million cell updates/sec

Title: US-10-738-413-1
Perfect score: 21
Sequence: 1 uaggaccugccagucucut 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 8033812

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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4	17	81.0	20	54	US-10-424-041-56	Sequence 56, Appl
5	17	81.0	20	54	US-10-424-041-144	Sequence 144, Appl
6	14.8	70.5	19	60	US-10-714-333A-239150	Sequence 239150, A
7	14.2	67.6	19	60	US-10-714-333A-62335	Sequence 62335, A
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9	14.2	67.6	19	60	US-10-714-333A-1492857	Sequence 1492857, A
10	13.8	65.7	19	60	US-10-714-333A-113284	Sequence 113284, A
11	13.8	65.7	19	60	US-10-714-333A-113286	Sequence 113286, A
12	13.8	65.7	21	62	US-10-770-726-7139	Sequence 7139, Ap
13	13.6	64.8	20	2	PCT-US03-37756-12	Sequence 49, Appl
14	13.6	64.8	20	52	US-10-304-082-11	Sequence 11, Appl
15	13.6	64.8	20	52	US-10-304-082-48	Sequence 48, Appl
16	13.6	64.8	21	63	PCT-US04-15645-2129	Sequence 2129, Ap
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ALIGNMENTS

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Sequence 1, Application US/10738413
GENERAL INFORMATION:
APPLICANT: BINETTI, RALPH R.
TITLE OF INVENTION: ST-RNA-MEDIATED GENE SILENCING TECHNOLOGY TO INHIBIT
FILE REFERENCE: SC66U-US
CURRENT APPLICATION NUMBER: US/10/738,413
CURRENT FILING DATE: 2003-12-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 1
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic
OTHER INFORMATION: oligonucleotide
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-738-413-1
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Best Local Similarity 100.0%; Pred. No. 9.2; Mismatches 0; Gaps 0;
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DB 1 UAGACCCGCGAGCUCUUT 21
RESULT 2
US-10-424-041-41/c
Sequence 41, Application US/10424041
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Thomas Condon
APPLICANT: Susan M. Freiler
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
FILE REFERENCE: BIOL0005US
CURRENT APPLICATION NUMBER: US/10/424,041
CURRENT FILING DATE: 2003-04-25
NUMBER OF SEQ ID NOS: 184
SEQ ID NO 41
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-424-041-41
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DB 18 TAGACCTCGCAGTGTCTC 1
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US-10-424-041-132
Sequence 132, Application US/10424041
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Thomas Condon
APPLICANT: Susan M. Freiler
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION

FILE REFERENCE: BIOL0005US
CURRENT APPLICATION NUMBER: US/10/424,041
CURRENT FILING DATE: 2003-04-25
NUMBER OF SEQ ID NOS: 184
SEQ ID NO 132
LENGTH: 20
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
US-10-424-041-132

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Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3 UAGACCGCCAGUCGUC 20

RESULT 4
US-10-424-041-56/c
Sequence 56, Application US/10424041
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Thomas Condon
APPLICANT: Susan M. Freiler
APPLICANT: Kenneth W. Doble
TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
FILE REFERENCE: BIOL0005US
CURRENT APPLICATION NUMBER: US/10/424,041
CURRENT FILING DATE: 2003-04-25
NUMBER OF SEQ ID NOS: 184
SEQ ID NO 56
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense oligonucleotide
US-10-424-041-56

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Sequence 144, Application US/10424041
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Thomas Condon
APPLICANT: Susan M. Freiler
APPLICANT: Kenneth W. Doble
TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
FILE REFERENCE: BIOL0005US
CURRENT APPLICATION NUMBER: US/10/424,041
CURRENT FILING DATE: 2003-04-25
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US-10-424-041-144

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RESULT 6
US-10-714-333A-239150
Sequence 239150, Application US/10714333A
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/10/714,333A
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 239150
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-10-714-333A-239150

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DB 2 GACCGCCAGUCGUCUU 19

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Sequence 62335, Application US/10714333A
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/10/714,333A
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
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PRIOR FILING DATE: 2002-11-14
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SOFTWARE: Proprietary
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TYPE: RNA
ORGANISM: Homo sapiens
US-10-714-333A-62335

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; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AML101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7139
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-7139

Query Match      65.7%; Score 13.8; DB 62; Length 21;
Best Local Similarity 70.6%; Pred. No. 3.9e+04;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 AGGACCCGCGCAGUCUC 18
Db      17 AGGACCTGCTGTGTTC 1

RESULT 13
PCT-US03-37756-12
; Sequence 12, Application PC/TUS0337756
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
; FILE REFERENCE: ISPT-1008
; CURRENT APPLICATION NUMBER: PCT/US03/37756
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,082
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US03-37756-12

Query Match      64.8%; Score 13.6; DB 2; Length 20;
Best Local Similarity 70.0%; Pred. No. 4.9e+04;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AGGACCCGCGCAGUCUC 21
Db      1 AGGACCTGCGAGGCTCAT 20

RESULT 14
PCT-US03-37756-49/c
; Sequence 49, Application PC/TUS0337756
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
; FILE REFERENCE: ISPT-1008
; CURRENT APPLICATION NUMBER: PCT/US03/37756
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,082
; PRIOR FILING DATE: 2002-11-22
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; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-37756-49

Query Match      64.8%; Score 13.6; DB 2; Length 20;
Best Local Similarity 70.0%; Pred. No. 4.9e+04;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AGGACCCGCGCAGUCUC 21
Db      20 AGGACCTGCGAGGCTCAT 1

RESULT 15
US-10-304-082-11
; Sequence 11, Application US/10304082
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
; FILE REFERENCE: PIS-0037
; CURRENT APPLICATION NUMBER: US/10/304,082
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-082-11

Query Match      64.8%; Score 13.6; DB 52; Length 20;
Best Local Similarity 70.0%; Pred. No. 4.9e+04;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AGGACCCGCGCAGUCUC 21
Db      1 AGGACCTGCGAGGCTCAT 20
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Search completed: September 17, 2005, 09:49:56
Job time : 2469 secs

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 08:05:35 ; Search time 1261 Seconds

(without alignments)
226.200 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 usagaccgcagcagucucut 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 24829634 seqs, 6791393036 residues

Total number of hits satisfying chosen parameters: 23489972

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Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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26: /cgn2_6/ptodata/1/pna/US04_39941-1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	2	Sequence 1, Appl
2	18	88.7	20	21	Sequence 12, Appl
3	18	88.7	20	21	Sequence 13, Appl
4	17.8	84.8	21	12	Sequence 344173
5	17.8	84.8	21	12	Sequence 344173
6	17.8	84.8	21	16	Sequence 682886
7	17	81.0	20	21	Sequence 682886

8	17	81.0	20	21	US-11-071-788-144	Sequence 144, App
9	16.4	78.1	21	11	US-10-604-985A-21186	Sequence 21186, A
10	16.4	78.1	21	12	US-10-604-985-21186	Sequence 21186, A
11	15.2	72.4	21	12	US-10-605-923-784389	Sequence 784389, A
12	15.2	72.4	21	13	US-10-605-924-964352	Sequence 964352, A
13	15.2	72.4	21	16	US-10-310-914A-964352	Sequence 964352, A
14	14.8	70.5	19	2	PCT-US03-36787-239150	Sequence 239150, A
15	14.8	70.5	19	14	US-10-714-333B-239150	Sequence 239150, A
16	14.8	70.5	19	22	US-11-083-784-239150	Sequence 239150, A
17	14.8	70.5	19	25	US-11-093-832-239150	Sequence 239150, A
18	14.8	70.5	19	25	US-11-101-244-239150	Sequence 239150, A
19	14.6	69.5	21	11	US-10-707-975B-452899	Sequence 452899, A
20	14.6	69.5	21	12	US-10-605-924-193827	Sequence 193827, A
21	14.6	69.5	21	16	US-10-310-914A-193827	Sequence 193827, A
22	14.4	68.6	17	11	US-10-707-975B-145451	Sequence 145451, A
23	14.4	68.6	17	12	US-10-605-923-1313526	Sequence 1313526, A
24	14.4	68.6	18	13	US-10-605-924-1315887	Sequence 1315887, A
25	14.4	68.6	18	16	US-10-310-914A-1315887	Sequence 1315887, A
26	14.4	68.6	19	13	US-10-605-924-1315888	Sequence 1315888, A
27	14.4	68.6	19	16	US-10-310-914A-1315888	Sequence 1315888, A
28	14.2	67.6	19	2	PCT-US03-36787-62335	Sequence 62335, A
29	14.2	67.6	19	2	PCT-US03-36787-1045669	Sequence 1045669, A
30	14.2	67.6	19	2	PCT-US03-36787-1492857	Sequence 1492857, A
31	14.2	67.6	19	14	US-10-714-333B-62335	Sequence 62335, A
32	14.2	67.6	19	14	US-10-714-333B-1045669	Sequence 1045669, A
33	14.2	67.6	19	14	US-10-714-333B-1492857	Sequence 1492857, A
34	14.2	67.6	19	22	US-11-083-784-62335	Sequence 62335, A
35	14.2	67.6	19	22	US-11-083-784-1045669	Sequence 1045669, A
36	14.2	67.6	19	22	US-11-083-784-1492857	Sequence 1492857, A
37	14.2	67.6	19	22	US-11-093-832-62335	Sequence 62335, A
38	14.2	67.6	19	23	US-11-093-832-1045669	Sequence 1045669, A
39	14.2	67.6	19	23	US-11-093-832-1492857	Sequence 1492857, A
40	14.2	67.6	19	24	US-11-095-383-62335	Sequence 62335, A
41	14.2	67.6	19	25	US-11-101-244-62335	Sequence 62335, A
42	14.2	67.6	19	25	US-11-101-244-1045669	Sequence 1045669, A
43	14.2	67.6	19	25	US-11-101-244-1492857	Sequence 1492857, A
44	14.2	67.6	21	11	US-10-707-975B-500017	Sequence 500017, A
45	14.2	67.6	21	12	US-10-605-923-327282	Sequence 327282, A

ALIGNMENTS

RESULT 1

PCT-US04-39941-1

Sequence 1, Application PC/TUS0439941

GENERAL INFORMATION:

APPLICANT: AVON PRODUCTS, INC.

TITLE OF INVENTION: TYROSINASE AND REDUCE PIGMENTATION

FILE REFERENCE: SC66U-WO

CURRENT FILING DATE: 2004-11-30

PRIOR APPLICATION NUMBER: 10/738,413

PRIOR FILING DATE: 2003-12-17

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 3.3

SEQ ID NO 1

LENGTH: 21

TYPE: DNA

ORGANISM: Artificial Sequence

OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic

FEATURE:

OTHER INFORMATION: oligonucleotide

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

PCT-US04-39941-1

Query Match 100.0%; Score 21; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LENGTH: 21
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-605-924-682886

Query Match 84.8%; Score 17.8; DB 12; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 14; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 UAGACCTGCCAGGCGCTT 21
Db 21 TGGAGCTGCGAGTGTCTGT 1

RESULT 6
US-10-310-914A-682886/c
Sequence 682886, Application US/10310914A
GENERAL INFORMATION:
APPLICANT: Benitich, Isaac
APPLICANT: Shiller, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 682886
LENGTH: 21
TYPE: RNA
ORGANISM: Human
US-10-310-914A-682886

Query Match 84.8%; Score 17.8; DB 16; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 14; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 UAGACCTGCCAGGCGCTT 21
Db 21 TGGAGCTGCGAGTGTCTGT 1

RESULT 7
US-11-071-788-56/c
Sequence 56, Application US/11071788
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Thomas Condon
APPLICANT: Susan M. Freiler
APPLICANT: James Karras
APPLICANT: Susan Fitch
APPLICANT: Ravi Jain
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
FILE REFERENCE: BNDL-0017US.P1
CURRENT APPLICATION NUMBER: US/11/071,788
CURRENT FILING DATE: 2005-03-02
PRIOR APPLICATION NUMBER: US 10/424,041
PRIOR FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 10/704,263
PRIOR FILING DATE: 2003-11-06
PRIOR APPLICATION NUMBER: US 10/889,101
PRIOR FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: US 60/486,652
PRIOR FILING DATE: 2003-07-12
PRIOR APPLICATION NUMBER: US 10/889,447
PRIOR FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: US 60/486,670
PRIOR FILING DATE: 2003-07-12
PRIOR APPLICATION NUMBER: US 10/498,704
PRIOR FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: PCT/US02/39873
PRIOR FILING DATE: 2002-12-13

PRIOR APPLICATION NUMBER: US 10/029,517
PRIOR FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 184
SEQ ID NO 56
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: Antisense Oligonucleotide
US-11-071-788-56

Query Match 81.0%; Score 17; DB 21; Length 20;
Best Local Similarity 76.5%; Pred. No. 3.6e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGACCTGCCAGGCGCU 17
Db 17 TAGGAGCTGCGAGTGTCT 1

RESULT 8
US-11-071-788-144
Sequence 144, Application US/11071788
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Thomas Condon
APPLICANT: Susan M. Freiler
APPLICANT: James Karras
APPLICANT: Susan Fitch
APPLICANT: Ravi Jain
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
FILE REFERENCE: BNDL-0017US.P1
CURRENT APPLICATION NUMBER: US/11/071,788
CURRENT FILING DATE: 2005-03-02
PRIOR APPLICATION NUMBER: US 10/424,041
PRIOR FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 10/704,263
PRIOR FILING DATE: 2003-11-06
PRIOR APPLICATION NUMBER: US 10/889,101
PRIOR FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: US 60/486,652
PRIOR FILING DATE: 2003-07-12
PRIOR APPLICATION NUMBER: US 10/889,447
PRIOR FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: US 60/486,670
PRIOR FILING DATE: 2003-07-12
PRIOR APPLICATION NUMBER: US 10/498,704
PRIOR FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: PCT/US02/39873
PRIOR FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US 10/029,517
PRIOR FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 184
SEQ ID NO 144
LENGTH: 20
TYPE: DNA
ORGANISM: M. musculus
FEATURE:
US-11-071-788-144

Query Match 81.0%; Score 17; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGACCTGCCAGGCGCU 17
Db 4 UAGACCTGCCAGGCGCU 20

RESULT 9
US-10-604-985A-21186
Sequence 21186, Application US/10604985A

```
1 GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55011
; CURRENT APPLICATION NUMBER: US/10/604,985A
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 97967
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21186
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Human
US-10-604-985A-21186
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Query Match 78.1%; Score 16.4; DB 11; Length 21;
Best Local Similarity 72.2%; Pred. No. 7.3e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 UAGACCCUGCCAGUCGUC 18
: |||||: |||||: |||||:
Db 4 TGGGACCTGCCAGTGTCTC 21
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```
RESULT 10
US-10-604-985-21186
; Sequence 21186, Application US/10604985
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55011
; CURRENT APPLICATION NUMBER: US/10/604,985
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 97947
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21186
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-604-985-21186
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Query Match 78.1%; Score 16.4; DB 12; Length 21;
Best Local Similarity 72.2%; Pred. No. 7.3e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 UAGACCCUGCCAGUCGUC 18
: |||||: |||||: |||||:
Db 4 TGGGACCTGCCAGTGTCTC 21
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RESULT 11
US-10-605-923-784389/C
; Sequence 784389, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 784389
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-784389
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Query Match 72.4%; Score 15.2; DB 12; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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Qy 1 UAGACCCUGCCAGUCGUC 20
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Db 21 TAGATCTCCAAAGTCTCTT 2
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RESULT 12
US-10-605-924-964352
; Sequence 964352, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 964352
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-964352
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Query Match 72.4%; Score 15.2; DB 13; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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```
Qy 1 UAGACCCUGCCAGUCGUC 20
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Db 1 TAGATCTCCAAAGTCTCTT 20
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```
RESULT 13
US-10-310-914A-964352
; Sequence 964352, Application US/10310914A
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kruszat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 964352
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-964352
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```
Query Match 72.4%; Score 15.2; DB 16; Length 21;
Best Local Similarity 80.0%; Pred. No. 2.9e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 UAGACCCUGCCAGUCGUC 20
: |||||: |||||: |||||:
Db 1 UAGAUUCUCCAAGUCUCU 20
```

```
RESULT 14
PCT-US03-36787-239150
; Sequence 239150, Application PC/TUS0336787
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leahe, Devin
; APPLICANT: Marshall, William
; APPLICANT: Read, Steven
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Methods and Compositions for Improving
; TITLE OF INVENTION: siRNA Functionality
```



```

; FILE REFERENCE: 1349PCT
; CURRENT APPLICATION NUMBER: PCT/US03/36787
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 239150
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
PCT-US03-36787-239150

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Query Match 70.5%; Score 14.8; DB 2; Length 19;
Best Local Similarity 77.8%; Pred. No. 4.6e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy 4 GACCUCCGAGUCUCUUTT 21
Db 2 GACCUCCGAGUCUCUUTT 19

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RESULT 15
US-10-714-333B-239150
; Sequence 239150, Application US/10714333B
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333B
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 239150
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333B-239150

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Query Match 70.5%; Score 14.8; DB 14; Length 19;
Best Local Similarity 77.8%; Pred. No. 4.6e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GACCUCCGAGUCUCUUTT 21
Db 2 GACCUCCGAGUCUCUUTT 19

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